

FIGURE 1

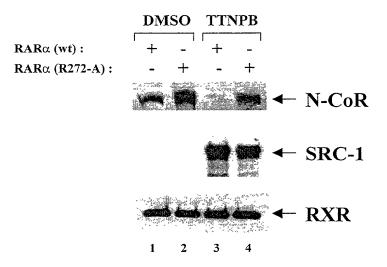


FIGURE 2A

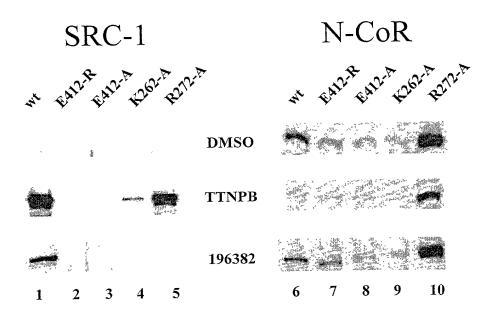
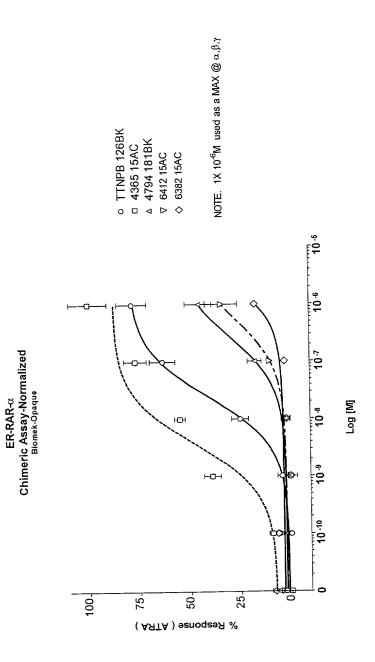


FIGURE 2B

FIGURE 3A



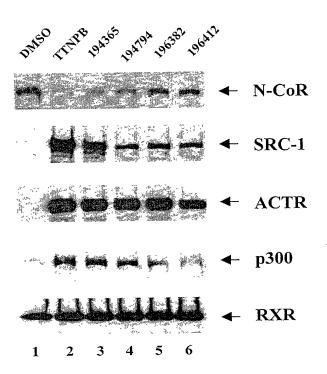


FIGURE 3B

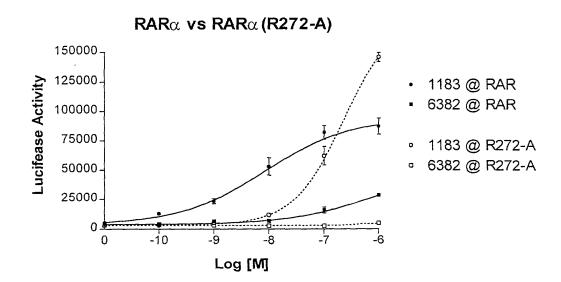


Figure 4

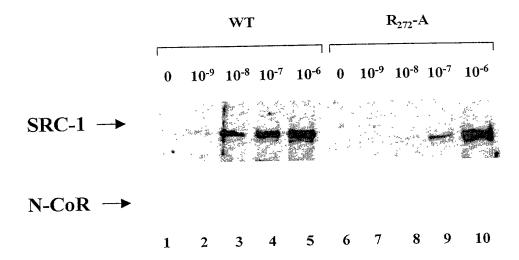


FIGURE 5A

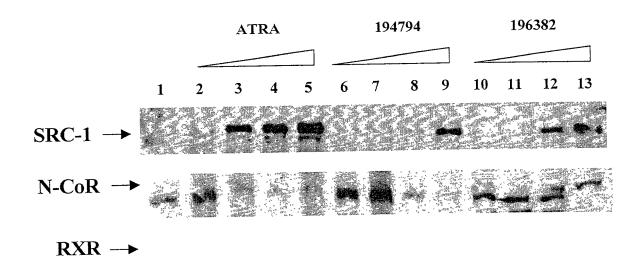
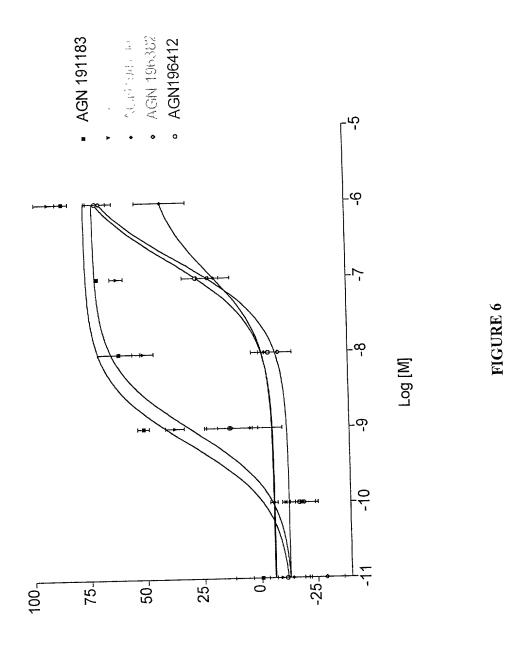


FIGURE 5B



% INHIBILION

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MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGALTTLQHQLPVSGYSTPSPATIE
TQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTC
HRDKNCIINKVTRNRCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGE
LIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVDFAKQLPG
FTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVF
AFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPH
MFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGRDG
GGLAPPPGSCSPSLSPSSNRSSPATHSP

FIGURE 7A

MFDCMDVLSVSPGQILDFYTASPSSCMLQEKALKACFSGLTQTEWQHRHTAQSIETQSTSSE
ELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCV
INKVTRNRCQYCRLQKCFEVGMSKESVRNDRNKKKKETSKQECTESYEMTAELDDLTEKIRK
AHQETFPSLCQLAKYTTNSSADHRVRLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLTIA
DQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFTFANQLL
PLEMDDTETGLLSAICLICGDRQDLEEPTKVDKLQEPLLEALKIYIRKRRPSKPHMFPKILM
KITDLRSISAKGAERVITLKMEIPGSMPPLIQEMMENSEGHEPLTPSSSGNTAEHSPSISPS
SVENSGVSQSPLVQ

FIGURE 7B

MATNKERLFAAGALGPGSGYPGAGFPFAFPGALRGSPPFEMLSPSFRGLGQPDLPKEMASLS
VETQSTSSEEMVPSSPSPPPPPRVYKPCFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKNMVY
TCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSKEAVRNDRNKKKKEVKEEGSPDSYELSPQL
EELITKVSKAHQETFPSLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAKRL
PGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDL
VFAFAGQLLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYARRRRPSQ
PYMFPRMLMKITDLRGISTKGAERAITLKMEIPGPMPPLIREMLENPEMFEDDSSQPGPHPN
ASSEDEVPGGQGKGGLKSPA

FIGURE 7C

Oimer N-terminus AF1 C4 Zn Fingers CTE E1 Contacts h9 AF2 C-terminus (hAXAa) hRXRα hRARY rTRαI hPPARy hERα hPR GM Ligand binding Domain. il - Contact i : 23 DNA Binding Domain: H P-Box == hRXRa GKHYGYYSTEGTKÖFFKETTÆXDL--TYTTERDNKDALIDKRORNETTYGRYOKTTAHEM JERXR VKHYGYFAJEGJKÖFFKESVENNE--KYSTLGKEH DTDKKSENNETTYGREGKTÖVÖVGM CTE GYHYRCIT, EGIKGFFRRIIQXNLHPSYSIKYEGKEVIDKYTRNO QEERFKRIIYXGMATDI.VLOQSKRIAKAKLIEENREK: GYHYGYWS GEGRAFFKRSIQGH--NDYNCPATNOTIDKNRRKSGOAFALRKTYEVGMMKGG GCHYGYLT GSGKYFFKRAVEGQ--HNYLCAGRNOGIIDKIRRKALPARYRKTOAGM hTRB (21) hERa (22) rGR N α-nelices 22.5 E1 Region Heptad 9 (h9) AF2 Domain φφχΦφφ hRXRa WARRIPH SELPLONVILL jfRXR WARRLPH ROLSIAN VVLL hRXRa FLMEML JFRXR FLLDML ${23} \\ {24}$ LULELEALR VILRIPALR (33)(43)(34)j FRXR (44)hTRa1 FAKKLPM SELPCEIDITLL HRARY FAKRLPG TGLSIADITLL HPPARY YAKSIPG VNLDLNT NTIL (25) (26) (27) HTRAI LLMKVTOLR HRAR, MLMKITOLR HPPAR, LLQKMTOLR hTRa1 LELEYF hRARY hPPARY $\binom{28}{29}$ **hLXR** (38) (39) HLXR MLMKLVSLR hLXR hVDR LL SEIW **hVDR hVDR** MIQKLADLR WAKRYPO VOLTLHOOVHLL WAKAIPO RNLHLOOMTLL WSKSLPO RNLHIOMITLI (30)LILEML hER hER hGR hPR hER hGR hPR LLLILSHIR (50) (51) (52) (31)hGR LTKLLDSMH LTKLLDNLH MLAHII MUSHVI (32)**hPR** a-helix 3 a-helix 4 cz-helix10/11 a-helix 12

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FIGURE 8